

AMENDMENT TO THE CLAIMS

Please amend the claims as follows:

Please cancel claims 2 to 26, 28 to 30, 32, 33, 35 to 37, 43, 44, 46, 47, 49, 51, 53, 55, 58, 61 to 90, 93, 94, 97, 99, 101, 105, 107, 113 to 115, 117 to 119, 123 to 125, 127 to 130, 132 to 140, 142 to 145, 147 to 161, 165 to 172, 174, 179, 182 to 186, 188, 190 to 196, 198, 207, 208, 212 and 214 to 220, without prejudice or disclaimer.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): An isolated, synthetic or recombinant nucleic acid comprising

(a) a nucleic acid sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more or complete (100%) sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID

NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377, SEQ ID NO:379, SEQ ID NO:381, SEQ ID NO:383, SEQ ID NO:385, SEQ ID NO:387, SEQ ID NO:389, SEQ ID NO:391, SEQ ID NO:393, SEQ ID NO:395, SEQ ID NO:397, SEQ ID NO:399, SEQ ID NO:401, SEQ ID NO:403, SEQ ID NO:405, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:411, SEQ ID NO:413, SEQ ID NO:415, SEQ ID NO:417, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:423, SEQ ID NO:425, SEQ ID NO:427, SEQ ID NO:429, SEQ ID NO:431, SEQ ID NO:433, SEQ ID NO:435, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:441, SEQ ID NO:443, SEQ ID NO:445, SEQ ID NO:447, SEQ ID NO:449, SEQ ID NO:451, SEQ ID NO:453, SEQ ID NO:455, SEQ ID NO:457, SEQ ID NO:459, SEQ ID NO:461, SEQ ID NO:463, SEQ ID NO:465, SEQ ID NO:467, SEQ ID NO:469, SEQ ID NO:471, SEQ ID NO:473, SEQ ID NO:475, SEQ ID NO:477, SEQ ID NO:479, SEQ ID NO:481, SEQ ID NO:483, SEQ ID NO:485, SEQ ID NO:487, SEQ ID NO:489, SEQ ID NO:491, SEQ ID NO:493, SEQ ID NO:495, SEQ ID

NO:497, SEQ ID NO:499, SEQ ID NO:501, SEQ ID NO:503, SEQ ID NO:505, SEQ ID NO:507, SEQ ID NO:509, SEQ ID NO:511, SEQ ID NO:513, SEQ ID NO:515 or SEQ ID NO:517, over a region of at least about 20, 30, 40, 50, 60, 75 or 100, or 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues, or over the full length of the gene or transcript, wherein the nucleic acid encodes at least one polypeptide having: (i) a glucanase, mannanase or xylanase activity, or (ii) immunogenic activity and can generate an antibody that specifically binds to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:144, SEQ ID NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272,

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SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302,
SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312,
SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322,
SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332,
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SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362,
SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372,
SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378, SEQ ID NO:380, SEQ ID NO:382,
SEQ ID NO:384, SEQ ID NO:386, SEQ ID NO:388, SEQ ID NO:390, SEQ ID NO:392,
SEQ ID NO:394, SEQ ID NO:396, SEQ ID NO:398, SEQ ID NO:400, SEQ ID NO:402,
SEQ ID NO:404, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:410, SEQ ID NO:412,
SEQ ID NO:414, SEQ ID NO:416, SEQ ID NO:418, SEQ ID NO:420, SEQ ID NO:422,
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SEQ ID NO:444, SEQ ID NO:446, SEQ ID NO:448, SEQ ID NO:450, SEQ ID NO:452,
SEQ ID NO:454, SEQ ID NO:456, SEQ ID NO:458, SEQ ID NO:460, SEQ ID NO:462,
SEQ ID NO:464, SEQ ID NO:466, SEQ ID NO:468, SEQ ID NO:470, SEQ ID NO:472,
SEQ ID NO:474, SEQ ID NO:476, SEQ ID NO:478, SEQ ID NO:480, SEQ ID NO:482,
SEQ ID NO:484, SEQ ID NO:486, SEQ ID NO:488, SEQ ID NO:490, SEQ ID NO:492,
SEQ ID NO:494, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:500, SEQ ID NO:502,
SEQ ID NO:504, SEQ ID NO:506, SEQ ID NO:508, SEQ ID NO:510, SEQ ID NO:512,
SEQ ID NO:514, SEQ ID NO:516 or SEQ ID NO:518; [[, and]]

(b) the nucleic acid sequence of (a), wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection;

(c) the nucleic acid sequence of (b), wherein the sequence comparison algorithm comprises a BLASTN program using as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands, and all other options are set to default;

(d) a nucleic acid sequence encoding a polypeptide having a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22,

SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:144, SEQ ID NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360,

SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370,
SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378, SEQ ID NO:380,
SEQ ID NO:382, SEQ ID NO:384, SEQ ID NO:386, SEQ ID NO:388, SEQ ID NO:390,
SEQ ID NO:392, SEQ ID NO:394, SEQ ID NO:396, SEQ ID NO:398, SEQ ID NO:400,
SEQ ID NO:402, SEQ ID NO:404, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:410,
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SEQ ID NO:422, SEQ ID NO:424, SEQ ID NO:426, SEQ ID NO:428, SEQ ID NO:430,
SEQ ID NO:432, SEQ ID NO:434, SEQ ID NO:436, SEQ ID NO:438, SEQ ID NO:440,
SEQ ID NO:442, SEQ ID NO:444, SEQ ID NO:446, SEQ ID NO:448, SEQ ID NO:450,
SEQ ID NO:452, SEQ ID NO:454, SEQ ID NO:456, SEQ ID NO:458, SEQ ID NO:460,
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SEQ ID NO:472, SEQ ID NO:474, SEQ ID NO:476, SEQ ID NO:478, SEQ ID NO:480,
SEQ ID NO:482, SEQ ID NO:484, SEQ ID NO:486, SEQ ID NO:488, SEQ ID NO:490,
SEQ ID NO:492, SEQ ID NO:494, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:500,
SEQ ID NO:502, SEQ ID NO:504, SEQ ID NO:506, SEQ ID NO:508, SEQ ID NO:510,
SEQ ID NO:512, SEQ ID NO:514, SEQ ID NO:516 or SEQ ID NO:518;

(e) a nucleic acid sequence that hybridizes under stringent conditions to a nucleic acid
comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ
ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21,
SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID
NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43,
SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID
NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65,
SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID
NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87,
SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID
NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID
NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID
NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID
NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID
NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID
NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID
NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID

NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID
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NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID
NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID
NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID
NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID
NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID
NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID
NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID
NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID
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NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID
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NO:439, SEQ ID NO:441, SEQ ID NO:443, SEQ ID NO:445, SEQ ID NO:447, SEQ ID
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NO:459, SEQ ID NO:461, SEQ ID NO:463, SEQ ID NO:465, SEQ ID NO:467, SEQ ID
NO:469, SEQ ID NO:471, SEQ ID NO:473, SEQ ID NO:475, SEQ ID NO:477, SEQ ID
NO:479, SEQ ID NO:481, SEQ ID NO:483, SEQ ID NO:485, SEQ ID NO:487, SEQ ID
NO:489, SEQ ID NO:491, SEQ ID NO:493, SEQ ID NO:495, SEQ ID NO:497, SEQ ID

NO:499, SEQ ID NO:501, SEQ ID NO:503, SEQ ID NO:505, SEQ ID NO:507, SEQ ID NO:509, SEQ ID NO:511, SEQ ID NO:513, SEQ ID NO:515 or SEQ ID NO:517,

wherein the nucleic acid encodes a polypeptide having a glucanase, mannanase or xylanase activity, the nucleic acid is at least about 20, 30, 40, 50, 60, 75, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more residues in length or the full length of the gene or transcript, and the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes;

(f) the nucleic acid of (a), (b), (c), (d) or (f), wherein the glucanase, mannanase or xylanase activity comprises: an endoglucanase activity; or catalyzing hydrolysis of 1,4-beta-D-glycosidic linkages or internal β -1,3-glucosidic linkages, or, hydrolyzing a glucan to produce a smaller molecular weight polysaccharide or oligomer; or an endoglucanase activity comprising an endo-1,4-beta-endoglucanase activity; or an endoglucanase activity comprising 1,4-beta-D-glycosidic linkage activity; or an endoglucanase activity comprising hydrolysis of a 1,4-beta-D-glycosidic linkage in a cellulose, a cellulose derivative, a lichenin or a cereal; or hydrolyzing a glycosidic linkage in a cellulose derivative; or hydrolyzing a glycosidic linkage in a carboxy methyl cellulose or a hydroxy ethyl cellulose; or hydrolyzing a glycosidic linkage in a cereal; or hydrolyzing a glycosidic linkage in a beta-D-glucan or a xyloglucan; or hydrolyzing polysaccharides comprising 1,4- β -glycoside-linked D-glucopyranoses; or hydrolyzing a cellulose, a cellulose derivative or a hemicellulose; or hydrolyzing a cellulose or a hemicellulose in a wood or paper pulp or a wood or paper product; or catalyzing hydrolysis of glucan in a feed, a food product or a beverage; or hydrolyzing a glucan in a feed, food product or beverage; hydrolyzing a glycosidic linkage or a glucan in a cereal-based animal feed, a wort or a beer, a dough, a fruit or a vegetable; or hydrolyzing a glucan in a microbial cell, a fungal cell, a mammalian cell or a plant cell;

(g) the nucleic acid of (a), (b), (c), (d), (e) or (f), wherein the glucanase, mannanase or xylanase activity is thermostable; or the polypeptide retains a glucanase, mannanase or xylanase activity under conditions comprising a temperature range of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C;

(h) the nucleic acid of (a), (b), (c), (d), (e) or (f), wherein the glucanase activity is thermotolerant; or the polypeptide retains a glucanase activity after exposure to a temperature in the range from greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C.

Claims 2 to 26 (canceled)

Claim 27 (currently amended): A nucleic acid probe for identifying a nucleic acid encoding a polypeptide with a glucanase activity, wherein the probe comprises at least 10 consecutive bases, or at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases, of a sequence comprising (a) SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID

NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377, SEQ ID NO:379, SEQ ID NO:381, SEQ ID NO:383, SEQ ID NO:385, SEQ ID NO:387, SEQ ID NO:389, SEQ ID NO:391, SEQ ID NO:393, SEQ ID NO:395, SEQ ID NO:397, SEQ ID NO:399, SEQ ID NO:401, SEQ ID NO:403, SEQ ID NO:405, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:411, SEQ ID NO:413, SEQ ID NO:415, SEQ ID NO:417, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:423, SEQ ID NO:425, SEQ ID NO:427, SEQ ID NO:429, SEQ ID NO:431, SEQ ID NO:433, SEQ ID NO:435, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:441, SEQ ID NO:443, SEQ ID NO:445, SEQ ID NO:447, SEQ ID NO:449, SEQ ID NO:451, SEQ ID NO:453, SEQ ID NO:455, SEQ ID NO:457, SEQ ID NO:459, SEQ ID NO:461, SEQ ID NO:463, SEQ ID NO:465, SEQ ID NO:467, SEQ ID NO:469, SEQ ID NO:471, SEQ ID NO:473, SEQ ID NO:475, SEQ ID NO:477, SEQ ID NO:479, SEQ ID NO:481, SEQ ID NO:483, SEQ ID NO:485, SEQ ID NO:487, SEQ ID NO:489, SEQ ID NO:491, SEQ ID NO:493, SEQ ID NO:495, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:501, SEQ ID NO:503, SEQ ID NO:505, SEQ ID NO:507, SEQ ID NO:509, SEQ ID NO:511, SEQ ID NO:513, SEQ ID NO:515 or SEQ ID NO:517, or (b) the sequence of claim 1, wherein the probe identifies the nucleic acid by binding or hybridization.

Claims 28 to 30 (canceled)

Claim 31 (currently amended): An amplification primer pair for amplifying a nucleic acid encoding a polypeptide having a glucanase, mannanase or xylanase activity, wherein the primer pair

(a) is capable of amplifying a nucleic acid comprising the [[a]] sequence of as set forth in claim 1 or claim 24, or a subsequence thereof, wherein a member of the amplification primer pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence, or, about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence; or,

(b) comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of the sequence of claim 1, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of the complementary strand of the first member.

Claims 32 to 33 (canceled)

Claim 34 (currently amended): A glucanase-encoding, mannanase-encoding or xylanase-encoding nucleic acid comprising: a nucleic acid generated by amplification of a polynucleotide using the [[an]] amplification primer pair of as set forth in claim 31 [[33]]; (b) the nucleic acid of (a), wherein the amplification is by polymerase chain reaction (PCR); (c) the nucleic acid of (b), wherein the nucleic acid is generated by amplification of a gene library; or (d) the nucleic acid of (c), wherein the gene library is an environmental library.

Claims 35 to 37 (canceled)

Claim 38 (currently amended): An isolated, synthetic or recombinant glucanase, mannanase or xylanase encoded by the [[a]] glucanase-encoding, mannanase-encoding or xylanase-encoding nucleic acid of as set forth in claim 34.

Claim 39 (currently amended): A method of amplifying a nucleic acid encoding a polypeptide having a glucanase, mannanase or xylanase activity comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying the [[a]] nucleic acid sequence of as set forth in claim 1 or claim 24, or a subsequence thereof.

Claim 40 (currently amended): An expression cassette comprising a nucleic acid comprising the [[a]] sequence of as set forth in claim 1 or claim 24.

Claim 41 (currently amended): A vector comprising a nucleic acid comprising the ~~[[a]] sequence of~~ as set forth in claim 1 or claim 24.

Claim 42 (currently amended): A cloning vehicle comprising (a) a nucleic acid comprising the ~~[[a]] sequence of as set forth in claim 1 or claim 24,~~ wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome; (b) the cloning vehicle of (a), wherein the viral vector comprises an adenovirus vector, a retroviral vector or an adeno-associated viral vector; (c) the cloning vehicle of (b), comprising a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

Claims 43 and 44 (canceled)

Claim 45 (currently amended): A transformed cell comprising (a) a nucleic acid comprising the ~~[[a]] sequence of as set forth in claim 1 or claim 24;~~ (b) an expression cassette as set forth in claim 40; or (c) the transformed cell of (a) or (b), wherein the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

Claims 46 and 47 (canceled)

Claim 48 (currently amended): A transgenic non-human animal comprising (a) the ~~[[a]] sequence of as set forth in claim 1 or claim 24;~~ or the transgenic non-human animal of (a), wherein the animal is a mouse.

Claim 49 (canceled)

Claim 50 (currently amended): A transgenic plant comprising (a) the ~~[[a]] sequence of as set forth in claim 1 or claim 24;~~ or, the transgenic plant of (a), wherein the plant is a corn plant, a sorghum plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant, a grass, or a tobacco plant.

Claim 51 (canceled)

Claim 52 (currently amended): A transgenic seed comprising (a) the [[a]] sequence of as set forth in claim 1 or claim 24; or, the transgenic seed of (a), wherein the seed is a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a rice, a barley, a peanut or a tobacco plant seed.

Claim 53 (canceled)

Claim 54 (currently amended): An antisense oligonucleotide comprising (a) a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to the [[a]] sequence of as set forth in claim 1 or claim 24, or a subsequence thereof; or, (b) the antisense oligonucleotide of (a), wherein the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

Claim 55 (canceled)

Claim 56 (currently amended): A method of inhibiting the translation of a glucanase, mannanase or xylanase message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to the [[a]] sequence of as set forth in claim 1 or claim 24.

Claim 57 (currently amended): A double-stranded inhibitory RNA (RNAi) molecule comprising (a) a subsequence of the [[a]] sequence of as set forth in claim 1 or claim 24; or, (b) the sequence of (a), wherein the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length.

Claim 58 (canceled)

Claim 59 (currently amended): A method of inhibiting the expression of a glucanase in a cell comprising administering to the cell or expressing in the cell a double-stranded

inhibitory RNA (iRNA), wherein the RNA comprises a subsequence of the [[a]] sequence of
~~as set forth in claim 1 or claim 24.~~

Claim 60 (currently amended): An isolated, synthetic or recombinant polypeptide
(i) having an amino acid sequence at least 50%, 51%, 52%, 53%, 54%, 55%, 56%,
57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%,
73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%,
89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more or complete (100%)
sequence identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID
NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20,
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SEQ ID NO:510, SEQ ID NO:512, SEQ ID NO:514, SEQ ID NO:516 or SEQ ID NO:518,
over a region of at least about 20, 25, 30, 35, 40, 45, 50, 55, 60, 75 or 100, 150, 200, 250, 300
or more residues, or over the full length of the polypeptide,

wherein the polypeptide has: (i) a glucanase, mannanase or xylanase activity, or (ii)
immunogenic activity and can generate an antibody that specifically binds to SEQ ID NO:2,
SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID
NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24,
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(ii) the amino acid sequence of (i), wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; [[, or, (ii)]]

(iii) the nucleic acid sequence of (b), wherein the sequence comparison algorithm comprises a BLAST version 2.2.2 algorithm having a filtering setting set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default;

(iv) an amino acid sequence encoded by the [[a]] nucleic acid of claim 1 having at least 50% sequence identity to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123,

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SEQ ID NO:505, SEQ ID NO:507, SEQ ID NO:509, SEQ ID NO:511, SEQ ID NO:513,
SEQ ID NO:515 or SEQ ID NO:517, over a region of at least about 20, 25, 30, 35, 40, 45, 50,
55, 60, 75 or 100 residues, and the sequence identities are determined by analysis with a
sequence comparison algorithm or by a visual inspection, or encoded by a nucleic acid
capable of hybridizing under stringent conditions to a sequence as set forth in SEQ ID NO:1,
SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID
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(v) the amino acid sequence of (i), (ii), (iii) or (iv) and having at least one conservative amino acid residue substitution and retaining a glucanase, mannanase or xylanase activity, wherein a conservative substitution comprises substituting an amino acid residue by another amino acid of like characteristics;

(vi) the amino acid sequence of (v), wherein the conservative substitution comprises replacement of an aliphatic amino acid with another aliphatic amino acid; or, replacement of a Serine with a Threonine or vice versa; or, replacement of an acidic residue with another acidic residue; or, replacement of a residue bearing an amide group with another residue bearing an amide group; or, exchange of a basic residue with another basic residue; or, replacement of an aromatic residue with another aromatic residue, or a combination thereof;

(vii) the amino acid sequence of (vi), wherein the aliphatic residue comprises Alanine, Valine, Leucine, Isoleucine or a synthetic equivalent thereof; or, the acidic residue comprises Aspartic acid, Glutamic acid or a synthetic equivalent thereof; or, the residue comprising an amide group comprises Aspartic acid, Glutamic acid or a synthetic equivalent thereof; or, the basic residue comprises Lysine, Arginine or a synthetic equivalent thereof; or, the aromatic residue comprises Phenylalanine, Tyrosine or a synthetic equivalent thereof;

(viii) the amino acid sequence of (i), (ii), (iii), (iv), (v), (vi) or (vii), wherein the glucanase, mannanase or xylanase activity comprises: an endoglucanase activity; or catalyzing hydrolysis of 1,4-beta-D-glycosidic linkages or internal β -1,3-glucosidic linkages, or, hydrolyzing a glucan to produce a smaller molecular weight polysaccharide or oligomer; or an endoglucanase activity comprising an endo-1,4-beta-endoglucanase activity; or an endoglucanase activity comprising 1,4-beta-D-glycosidic linkage activity; or an endoglucanase activity comprising hydrolysis of a 1,4-beta-D-glycosidic linkage in a cellulose, a cellulose derivative, a lichenin or a cereal; or hydrolyzing a glycosidic linkage in a cellulose derivative; or hydrolyzing a glycosidic linkage in a carboxy methyl cellulose or a hydroxy ethyl cellulose; or hydrolyzing a glycosidic linkage in a cereal; or hydrolyzing a glycosidic linkage in a beta-D-glucan or a xyloglucan; or hydrolyzing polysaccharides comprising 1,4- β -glycoside-linked D-glucopyranoses; or hydrolyzing a cellulose, a cellulose derivative or a hemicellulose; or hydrolyzing a cellulose or a hemicellulose in a wood or paper pulp or a wood or paper product; or catalyzing hydrolysis of glucan in a feed, a food product or a beverage; or hydrolyzing a glucan in a feed, food product or beverage; hydrolyzing a glycosidic linkage or a glucan in a cereal-based animal feed, a wort or a beer, a dough, a fruit or a vegetable; or hydrolyzing a glucan in a microbial cell, a fungal cell, a mammalian cell or a plant cell;

(ix) the amino acid sequence of (i), (ii), (iii), (iv), (v), (vi), (vii) or (viii), wherein the glucanase, mannanase or xylanase activity is thermostable; or the polypeptide retains a glucanase, mannanase or xylanase activity under conditions comprising a temperature range

of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C;

(x) the amino acid sequence of (i), (ii), (iii), (iv), (v), (vi), (vii) or (viii), wherein the glucanase activity is thermotolerant; or the polypeptide retains a glucanase activity after exposure to a temperature in the range from greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C;

(xi) the amino acid sequence of (i), (ii), (iii), (iv), (v), (vi), (vii), (viii), (ix) or (x), wherein the glucanase activity comprises a specific activity at about 37°C in the range from about 100 to about 1000 units per milligram of protein, from about 500 to about 750 units per milligram of protein, from about 500 to about 1200 units per milligram of protein, or from about 750 to about 1000 units per milligram of protein;

(xii) the amino acid sequence of (x), wherein the thermotolerance comprises retention of at least half of the specific activity of the glucanase at 37°C after being heated to an elevated temperature, or, the thermotolerance comprises retention of specific activity at 37°C in the range from about 500 to about 1200 units per milligram of protein after being heated to an elevated temperature;

(xiii) the amino acid sequence of any of (i) through (xii), wherein the polypeptide comprises at least one glycosylation site; or, wherein the polypeptide comprises at least one N-linked glycosylation site, or, wherein the polypeptide is glycosylated after being expressed in a *P. pastoris* or a *S. pombe*;

(xiv) the amino acid sequence of any of (i) through (xiii), wherein the polypeptide retains a glucanase activity under conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0; or, the polypeptide retains a glucanase activity under conditions comprising about pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5;

(xiv) the amino acid sequence of any of (i) through (xiii), wherein the polypeptide lacks a signal sequence or a prepro sequence;

(xv) the amino acid sequence of any of (i) through (xiv), and having a heterologous signal sequence or a heterologous prepro sequence, or having a yeast signal sequence; or

(xv) the amino acid sequence of any of (i) through (xiv), and having: (a) a heterologous sequence, or (b) a heterologous sequence not naturally associated with a glucanase, mannanase, or xylanase.

Claims 61 to 90 (canceled)

Claim 91 (currently amended): A protein preparation comprising the ~~the~~ [[a]] polypeptide of as set forth in claim 60, wherein the protein preparation comprises a liquid, a solid or a gel.

Claim 92 (currently amended): A heterodimer comprising: (a) the ~~the~~ [[a]] polypeptide of as set forth in claim 60 and a second domain; the heterodimer of (a), wherein the second domain is a polypeptide and the heterodimer is a fusion protein; or (c) the heterodimer of (a) or (b), wherein the second domain is an epitope or a tag.

Claims 93 to 94 (canceled)

Claim 95 (currently amended): A homodimer comprising the ~~the~~ [[a]] polypeptide of as set forth in claim 60.

Claim 96 (currently amended): An immobilized polypeptide, wherein the polypeptide comprises: (a) the ~~the~~ [[a]] sequence of as set forth in claim 60, or a subsequence thereof; or, (b) the immobilized polypeptide of (a), wherein the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

Claim 97 (canceled)

Claim 98 (currently amended): An array comprising: (a) an immobilized polypeptide comprising the amino acid sequence of as set forth in claim 60; or (b) an immobilized nucleic acid comprising the nucleic acid sequence of claim 1; or (c) a combination thereof.

Claim 99 (canceled)

Claim 100 (currently amended): An isolated, synthetic or recombinant antibody (a) that specifically binds to the ~~the~~ [[a]] polypeptide of as set forth in claim 60; or (b) the antibody of (a), wherein the antibody is a monoclonal or a polyclonal antibody.

Claim 101 (canceled)

Claim 102 (currently amended): A hybridoma comprising an antibody that specifically binds to the [[a]] polypeptide of ~~as set forth in~~ claim 60.

Claim 103 (currently amended): A method of isolating or identifying a polypeptide with a glucanase, mannanase or xylanase activity comprising the steps of:

- (a) providing the [[an]] antibody of ~~as set forth in~~ claim 100;
- (b) providing a sample comprising polypeptides; and
- (c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having a glucanase, mannanase or xylanase activity.

Claim 104 (currently amended): A method of making an anti-glucanase, anti-mannanase or anti-xylanase antibody comprising (a) administering to a non-human animal the [[a]] nucleic acid of ~~as set forth in claim 1 or claim 24 or a subsequence thereof~~ in an amount sufficient to generate a humoral immune response, thereby making an anti-glucanase, anti-mannanase or anti-xylanase antibody; or, (b) administering to a non-human animal the polypeptide of claim 60 in an amount sufficient to generate a humoral immune response, thereby making an anti-glucanase, anti-mannanase or anti-xylanase antibody.

Claim 105 (canceled)

Claim 106 (currently amended): A method of producing a recombinant polypeptide comprising the steps of:

- (A) (a) providing a nucleic acid operably linked to a promoter, wherein the nucleic acid comprises the [[a]] sequence of ~~as set forth in claim 1 or claim 24~~; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide; or
- (B) the method of (A), further comprising transforming a host cell with the nucleic acid of step (A) (a) followed by expressing the nucleic acid of step (A) (a), thereby producing a recombinant polypeptide in a transformed cell.

Claim 107 (canceled)

Claim 108 (currently amended): A method for identifying a polypeptide having a glucanase, mannanase or xylanase activity comprising the following steps:

- (a) providing the [[a]] polypeptide of as set forth in claim 60 [[64]];
- (b) providing a glucanase, mannanase or xylanase substrate; and
- (c) contacting the polypeptide with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having a glucanase, mannanase or xylanase activity.

Claim 109 (currently amended): A method for identifying a glucanase, mannanase or xylanase substrate comprising the following steps:

- (a) providing the [[a]] polypeptide of as set forth in claim 60 [[64]];
- (b) providing a test substrate; and
- (c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of a reaction product identifies the test substrate as a glucanase, mannanase or xylanase substrate.

Claim 110 (currently amended): A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

- (a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid has the [[a]] sequence of as set forth in claim 1 or claim 24;
- (b) providing a test compound;
- (c) contacting the polypeptide with the test compound; and
- (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

Claim 111 (currently amended): A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

- (a) providing the [[a]] polypeptide of ~~as set forth in~~ claim 60;
- (b) providing a test compound;
- (c) contacting the polypeptide with the test compound; and
- (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

Claim 112 (currently amended): A method for identifying a modulator of a glucanase, mannanase or xylanase activity comprising the following steps:

- (A) (a) providing the [[a]] polypeptide of ~~as set forth in~~ claim 60 [[64]];
- (b) providing a test compound;
- (c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the glucanase, wherein a change in the glucanase, mannanase or xylanase activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the glucanase, mannanase or xylanase activity; or

(B) the method of (A), wherein the glucanase, mannanase or xylanase activity is measured by providing a glucanase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product; or

(C) the method of (B), wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of a glucanase, mannanase or xylanase activity; or, wherein an increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of a glucanase, mannanase or xylanase activity.

Claims 113 to 115 (canceled)

Claim 116 (currently amended): A computer system comprising

- (A) a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence

comprises the sequence of as set forth in claim 60, or a polypeptide encoded by the [[a]] nucleic acid of as set forth in claim 1 or claim 24;

(B) the computer system of (A), further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon;

(C) the computer system of (B), wherein the sequence comparison algorithm comprises a computer program that indicates polymorphisms; or

(D) the computer system of (A), (B) or (C), further comprising an identifier that identifies one or more features in said sequence.

Claims 117 to 119 (canceled)

Claim 120 (currently amended): A computer readable medium having stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises the [[a]] polypeptide of as set forth in claim 60; or a polypeptide encoded by the [[a]] nucleic acid of as set forth in claim 1 or claim 24.

Claim 121 (currently amended): A method for identifying a feature in a sequence comprising the steps of: (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises the [[a]] polypeptide of as set forth in claim 60; or a polypeptide encoded by the [[a]] nucleic acid of as set forth in claim 1 or claim 24; and (b) identifying one or more features in the sequence with the computer program.

Claim 122 (currently amended): A method for comparing a first sequence to a second sequence comprising the steps of:

(A) (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises the [[a]] polypeptide of as set forth in claim 60; or a polypeptide encoded by the [[a]] nucleic acid of as set forth in claim 1 or claim 24; and (b) determining differences between the first sequence and the second sequence with the computer program;

(B) the method of (A), wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms;

(C) the method of (B), further comprising an identifier that identifies one or more features in a sequence;

(D) the method of (A), (B) or (C), comprising reading the first sequence using a computer program and identifying one or more features in the sequence.

Claims 123 to 125 (canceled)

Claim 126 (currently amended): A method for isolating or recovering a nucleic acid encoding a polypeptide with a glucanase, mannanase or xylanase activity from an environmental sample comprising the steps of:

(A) (a) providing the [[an]] amplification primer sequence pair of as set forth in claim 31 or claim 33;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide with a glucanase, mannanase or xylanase activity from an environmental sample;

(B) the method of (A), wherein each member of the amplification primer pair comprises an oligonucleotide comprising at least about 10 to 50, or about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of, the sequence of claim 1;

(C) (a) providing a polynucleotide probe comprising the sequence of claim 1;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with a glucanase, mannanase or xylanase activity from an environmental sample; or

(D) the method of (A), (B) or (C), wherein the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample, or, wherein the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

Claims 127 to 130 (canceled)

Claim 131 (currently amended): A method of generating a variant of a nucleic acid encoding a polypeptide with a glucanase, mannanase or xylanase activity comprising the steps of:

(A) (a) providing a template nucleic acid comprising the [[a]] sequence of as set forth in claim 1 or claim 24; and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid; or

(B) the method of (A), further comprising expressing the variant nucleic acid to generate a variant glucanase, mannanase or xylanase polypeptide;

(C) the method of claim (A) or (B), wherein the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis™ (GSSM™), synthetic ligation reassembly (SLR), recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation, or any combination thereof; or

(D) the method of (A) or (B) iteratively repeated until a glucanase, mannanase or xylanase having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced;

(E) the method of (A), (B), (C) or (D), wherein the variant glucanase, mannanase or xylanase polypeptide is thermotolerant, and retains some activity after being exposed to an elevated temperature;

(F) the method of (A), (B), (C) or (D), wherein the variant glucanase, mannanase or xylanase polypeptide has increased glycosylation as compared to the glucanase, mannanase or xylanase encoded by a template nucleic acid;

(G) the method of (A), (B), (C) or (D), wherein the variant glucanase, mannanase or xylanase polypeptide has a glucanase activity under a high temperature, wherein the glucanase, mannanase or xylanase encoded by the template nucleic acid is not active under the high temperature;

(H) the method of (A), (B), (C) or (D), wherein the method is iteratively repeated until a glucanase, mannanase or xylanase coding sequence having an altered codon usage from that of the template nucleic acid is produced; or

(I) the method of (A), (B), (C) or (D), wherein the method is iteratively repeated until a glucanase, mannanase or xylanase gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

Claims 132 to 140 (canceled)

Claim 141 (currently amended): A method for modifying codons in a nucleic acid encoding a polypeptide with a glucanase, mannanase or xylanase activity to increase or decrease its expression in a host cell, the method comprising the following steps:

(A) (a) providing a nucleic acid encoding a polypeptide with a glucanase, mannanase or xylanase activity comprising a sequence as set forth in claim 1 ~~or claim 24~~; and,

(b) identifying a non-preferred ~~non-Exemplary~~ or a less preferred ~~Exemplary~~ codon in the nucleic acid of step (a) and replacing it with a preferred ~~Exemplary~~ or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred ~~Exemplary~~ codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred ~~Exemplary~~ or less preferred ~~Exemplary~~ codon is a codon under-represented in

coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell;

(B) (a) providing a nucleic acid encoding a polypeptide with a glucanase activity comprising the sequence of claim 1; and,

(b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a glucanase; or,

(C) (a) providing a nucleic acid encoding a glucanase polypeptide comprising the sequence of claim 1; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non- preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell;

(D) (a) providing a nucleic acid encoding a glucanase polypeptide comprising the sequence of claim 1; and

(b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non- preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell; or,

(E) the method of (A), (B), (C) or (D), wherein the host cell is a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

Claims 142 to 145 (canceled)

Claim 146 (currently amended): A method for producing a library of nucleic acids encoding a plurality of modified glucanase, mannanase or xylanase active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps:

(A) (a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to ~~[[a]] the sequence of claim 1 as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311,~~

~~SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377, SEQ ID NO:379, SEQ ID NO:381, SEQ ID NO:383, SEQ ID NO:385, SEQ ID NO:387, SEQ ID NO:389, SEQ ID NO:391, SEQ ID NO:393, SEQ ID NO:395, SEQ ID NO:397, SEQ ID NO:399, SEQ ID NO:401, SEQ ID NO:403, SEQ ID NO:405, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:411, SEQ ID NO:413, SEQ ID NO:415, SEQ ID NO:417, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:423, SEQ ID NO:425, SEQ ID NO:427, SEQ ID NO:429, SEQ ID NO:431, SEQ ID NO:433, SEQ ID NO:435, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:441, SEQ ID NO:443, SEQ ID NO:445, SEQ ID NO:447, SEQ ID NO:449, SEQ ID NO:451, SEQ ID NO:453, SEQ ID NO:455, SEQ ID NO:457, SEQ ID NO:459, SEQ ID NO:461, SEQ ID NO:463, SEQ ID NO:465, SEQ ID NO:467, SEQ ID NO:469, SEQ ID NO:471, SEQ ID NO:473, SEQ ID NO:475, SEQ ID NO:477, SEQ ID NO:479, SEQ ID NO:481, SEQ ID NO:483, SEQ ID NO:485, SEQ ID NO:487, SEQ ID NO:489, SEQ ID NO:491, SEQ ID NO:493, SEQ ID NO:495, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:501, SEQ ID NO:503, SEQ ID NO:505, SEQ ID NO:507, SEQ ID NO:509, SEQ ID NO:511, SEQ ID NO:513, SEQ ID NO:515 or SEQ ID NO:517, or a subsequence thereof, and the nucleic acid encodes a glucanase active site or a glucanase substrate binding site;~~

(b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,

(c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified glucanase active sites or substrate binding sites;

(B) the method of (A), comprising mutagenizing the first nucleic acid of step (a) by a method comprising an optimized directed evolution system, Gene Site-Saturation MutagenesisTM (GSSMTM), or a synthetic ligation reassembly (SLR); or

(C) the method of (A), comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site-Saturation Mutagenesis™ (GSSM™), synthetic ligation reassembly (SLR), recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation, or a combination thereof.

Claims 147 to 161 (canceled)

Claim 162 (currently amended): An isolated, synthetic or recombinant signal sequence comprising, or consisting of, the [[a]] sequence of claim 60 or a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43 or 1 to 44, of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID

NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152,
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SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182,
SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192,
SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202,
SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212,
SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222,
SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232,
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SEQ ID NO:424, SEQ ID NO:426, SEQ ID NO:428, SEQ ID NO:430, SEQ ID NO:432,
SEQ ID NO:434, SEQ ID NO:436, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:442,
SEQ ID NO:444, SEQ ID NO:446, SEQ ID NO:448, SEQ ID NO:450, SEQ ID NO:452,
SEQ ID NO:454, SEQ ID NO:456, SEQ ID NO:458, SEQ ID NO:460, SEQ ID NO:462,
SEQ ID NO:464, SEQ ID NO:466, SEQ ID NO:468, SEQ ID NO:470, SEQ ID NO:472,

SEQ ID NO:474, SEQ ID NO:476, SEQ ID NO:478, SEQ ID NO:480, SEQ ID NO:482, SEQ ID NO:484, SEQ ID NO:486, SEQ ID NO:488, SEQ ID NO:490, SEQ ID NO:492, SEQ ID NO:494, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:500, SEQ ID NO:502, SEQ ID NO:504, SEQ ID NO:506, SEQ ID NO:508, SEQ ID NO:510, SEQ ID NO:512, SEQ ID NO:514, SEQ ID NO:516 or SEQ ID NO:518; or, comprising, or consisting of a sequence as set forth in Table 3.

Claim 163 (currently amended): A chimeric polypeptide comprising

(A) at least a first domain comprising signal peptide (SP) having the [[a]] sequence of ~~as set forth in~~ claim 162, and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP);

(B) the chimeric polypeptide of (A), wherein the heterologous polypeptide or peptide is not a glucanase, a mannanase or a xylanase, or an endoglucanase; or

(C) the chimeric polypeptide of (B), wherein the heterologous polypeptide or peptide is amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP) or a glucanase, a mannanase or a xylanase, or an endoglucanase catalytic domain (CD).

Claim 164 (currently amended): An isolated, synthetic or recombinant nucleic acid encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP) having the [[a]] sequence of ~~as set forth in~~ claim 162 and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

Claims 165 to 172 (canceled)

Claim 173 (currently amended): A method for hydrolyzing, breaking up or disrupting a glucan-comprising composition comprising the following steps:

(A) (a) providing the [[a]] polypeptide having a glucanase activity of ~~as set forth in~~ claim 60 [[64]], or a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or~~ ~~claim 24~~;

(b) providing a composition comprising a glucan; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the glucanase hydrolyzes, breaks up or disrupts the glucan- comprising composition; or

(B) the method of (A), wherein the composition comprises a plant cell, a bacterial cell, a yeast cell, an insect cell, or an animal cell.

Claim 174 (canceled)

Claim 175 (currently amended): A dough or a bread product comprising the ~~[[a]]~~ polypeptide of ~~as set forth in claim 60~~ ~~[[64]]~~.

Claim 176 (currently amended): A method of dough conditioning comprising contacting a dough or a bread product with at least one polypeptide of ~~as set forth in claim 60~~ ~~[[64]]~~ under conditions sufficient for conditioning the dough.

Claim 177 (currently amended): A beverage comprising the ~~[[a]]~~ polypeptide of ~~as set forth in claim 60~~ ~~[[64]]~~.

Claim 178 (currently amended): A method of beverage production comprising
(A) administration of at least one polypeptide of ~~as set forth in claim 60~~ ~~[[64]]~~ to a beverage or a beverage precursor under conditions sufficient for decreasing the viscosity of the beverage; or

(B) the method of (A), wherein the beverage or beverage precursor is a wort or a beer.

Claim 179 (canceled)

Claim 180 (currently amended): A food, a feed or a nutritional supplement comprising the ~~[[a]]~~ polypeptide of ~~as set forth in claim 60~~ ~~[[64]]~~.

Claim 181 (currently amended): A method for utilizing a glucanase, mannanase or xylanase as a nutritional supplement in an animal diet, the method comprising:

(A) preparing a nutritional supplement containing a glucanase, mannanase or xylanase enzyme comprising at least thirty contiguous amino acids of a polypeptide as set forth in claim 60 [[64]]; and

administering the nutritional supplement to an animal to increase utilization of a xylan contained in a feed or a food ingested by the animal;

(B) the method of (A), wherein the animal is a human;

(C) the method of (A), wherein the animal is a ruminant or a monogastric animal;

(D) the method of (A), (B) or (C), wherein the glucanase, mannanase or xylanase enzyme is prepared by expression of a polynucleotide encoding the glucanase in an organism selected from the group consisting of a bacterium, a yeast, a plant, an insect, a fungus and an animal; or

(E) the method of (A), (B), (C) or (D), wherein the organism is selected from the group consisting of an *S. pombe*, *S. cerevisiae*, *Pichia pastoris*, *E. coli*, *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

Claims 182 to 186 (canceled)

Claim 187 (currently amended): An edible enzyme delivery matrix comprising
(a) a thermostable recombinant glucanase, mannanase or xylanase enzyme; or
(b) the edible enzyme delivery matrix of (a) comprising the polypeptide of claim 60.

Claim 188 (canceled)

Claim 189 (currently amended): A method for delivering a glucanase, mannanase or xylanase supplement to an animal, the method comprising:

(a) preparing an edible enzyme delivery matrix in the form of pellets comprising a granulate edible carrier and a thermostable recombinant glucanase, mannanase or xylanase enzyme, wherein the pellets readily disperse the glucanase, mannanase or xylanase enzyme contained therein into aqueous media, and

administering the edible enzyme delivery matrix to the animal;

(b) the method of (a), wherein the recombinant glucanase, mannanase or xylanase enzyme comprises the polypeptide of claim 60;

(c) the method of (a) or (b), wherein the granulate edible carrier comprises a carrier comprising a grain germ, a grain germ that is spent of oil, a hay, an alfalfa, a timothy, a soy hull, a sunflower seed meal, a wheat midd or a combination thereof;

(d) the method of (a), (b) or (c), wherein the edible carrier comprises grain germ that is spent of oil;

(e) the method of (a), (b), (c) or (d), wherein the glucanase, mannanase or xylanase enzyme is glycosylated to provide thermostability at pelletizing conditions;

(f) the method of (a), (b), (c), (d) or (e), wherein the delivery matrix is formed by pelletizing a mixture comprising a grain germ and a glucanase, mannanase or xylanase;

(g) the method of (a), (b), (c), (d), (e) or (f), wherein the pelletizing conditions include application of steam;

(h) the method of (a), (b), (c), (d), (e), (f) or (g), wherein the pelletizing conditions comprise application of a temperature in excess of about 80°C for about 5 minutes and the enzyme retains a specific activity of at least 350 to about 900 units per milligram of enzyme.

Claims 190 to 196 (canceled)

Claim 197 (currently amended): An isolated, synthetic or recombinant nucleic acid comprising

(a) a sequence encoding a polypeptide having a glucanase, mannanase or xylanase activity and a signal sequence, wherein the nucleic acid comprises the [[a]] sequence of as set forth in claim 1; or

(b) the nucleic acid of (a), wherein the signal sequence is derived from another glucanase, mannanase or xylanase or a non-glucanase, mannanase or xylanase enzyme.

Claim 198 (canceled)

Claim 199 (currently amended): An isolated, synthetic or recombinant nucleic acid comprising a sequence encoding a polypeptide having a glucanase, mannanase or xylanase activity, wherein the sequence does not contain a signal sequence and the nucleic acid comprises a sequence of as set forth in claim 1.

Claim 200 (currently amended): A cellulose- or cellulose derivative- composition comprising the ~~[[a]]~~ polypeptide of as-set forth in claim 60 ~~[[64]]~~.

Claim 201 (currently amended): A wood, wood pulp or wood product comprising the ~~[[a]]~~ polypeptide of as-set forth in claim 60 ~~[[64]]~~.

Claim 202 (currently amended): A paper, paper pulp or paper product comprising the ~~[[a]]~~ polypeptide of as-set forth in claim 60 ~~[[64]]~~.

Claim 203 (currently amended): A method for reducing lignin in a paper, a wood or wood product comprising contacting the paper, wood or wood product with the ~~[[a]]~~ polypeptide of as-set forth in claim 60 ~~[[64]]~~.

Claim 204 (currently amended): A detergent composition comprising a polypeptide as set forth in claim 60 ~~[[64]]~~.

Claim 205 (currently amended): A pharmaceutical composition comprising the ~~[[a]]~~ polypeptide of as-set forth in claim 60 ~~[[64]]~~.

Claim 206 (currently amended): A method for eliminating or protecting animals from a microorganism comprising

(a) a glucan comprising administering the ~~[[a]]~~ polypeptide of as-set forth in claim 60 ~~[[64]]~~;

(b) the method of (a), wherein the microorganism is a bacterium; or

(c) the method of (b), wherein the bacterium is a *Salmonellae*.

Claims 207 to 208 (canceled)

Claim 209 (currently amended): A fuel comprising the ~~[[a]]~~ polypeptide of as-set forth in claim 60 ~~[[64]]~~.

Claim 210 (currently amended): A method for making a fuel comprising contacting a fermentable sugar with the ~~[[a]]~~ polypeptide of as-set forth in claim 60 ~~[[64]]~~.

Claim 211 (currently amended): A dairy product comprising:

(a) the [[a]] polypeptide of ~~as set forth in~~ claim 60 [[64]]; or

(b) the dairy product of (a), comprising a milk, an ice cream, a cheese or a yogurt.

Claim 212 (canceled)

Claim 213 (currently amended): A method for improving texture and flavor of a dairy product comprising the following steps: (a) providing the [[a]] polypeptide of ~~the invention as set forth in~~ claim 60 [[64]]; (b) providing a dairy product; and (c) contacting the polypeptide of step (a) and the dairy product of step (b) under conditions wherein the glucanase can improve the texture or flavor of the dairy product.

Claims 214 to 220 (canceled)